

AGAGTAGGATGCTGCTGAAGTCATCCATCAGGTGAAGAAGCACCTTGATACAGATGAGAAGGAGATGCT  
K S R M S A E V I H Q V E E A L D I D E K E M L 70  
GCCTCTTTTGTGCCGGGATGTTGCTATAGATGTGGTTCACCTAATGTCAGGGACCTTCTGGATATTTA  
140  
L F L C R D V A I D V V P P N V R D L L D I L  
CGGGAAGAGGTAAGCTGTCTGTCGGGACTTGGCTGAACCTGCTCTACAGAGTGAGGCGATTIGACCTGC  
210  
R E R G K L S V G D L A E L L Y R V R R F D L  
TCAAACGATCTTGAAGATGGACAGAAAAGCTGIGGAGACCCACCTGCTCAGGAACCCCTCACCTTGTTC  
280  
L K R I L K M D R K A V E T H L L R N P H L V S  
GGACTATAGAGTGCTGATGTCAGAGATTGGTGA 313  
D Y R V L M S E I G E

DEED

Fig. 1

Fig. 2

ATGCTCTGAAGTCATCCATCAGGTTGAAGAAGCACCTTGATACAGATGAGAAGGAGATGCTGCTCTTTTGTGCCGGGATGTTGCTATAGATGTGGTTCCACCTAAAGT 110  
 Met Ser Ala Glu Val Ile His Gln Val Glu Glu Ala Leu Asp Thr Asp Glu Lys Glu Met Leu Leu Phe Leu Cys Arg Asp Val Ala Ile Asp Val Val Pro Asn Val  
  
 CAGGGACCTTCTGGATATTTTACGGGAAAGAGGTAAAGCTGTCTGTGGGACTTGGCTGAACCTGCTCTACAGAGTGAGGCGATTTGACCTGCTCAAAACGTATCTTGAAGA 220  
 Arg Asp Leu Leu Asp Ile Leu Arg Glu Arg Gly Lys Leu Ser Val Gly Asp Leu Ala Glu Leu Leu Tyr Arg Val Arg Arg Phe Asp Leu Leu Lys Arg Ile Leu Lys  
  
 TGGACAGAAAAAGCTGTGGAGACCCACCTGCTCAGGAACCCCTACCTTGTTTCGGACTATAGAGTGTGATGGCAGAGATTTGGAGGATTTGGATAAATCTGATGTGTCC 330  
 Met Asp Arg Lys Ala Val Glu Thr His Leu Leu Arg Asn Pro His Leu Val Ser Asp Tyr Arg Val Leu Met Ala Glu Ile Gly Glu Asp Leu Asp Lys Ser Asp Val Ser  
  
 TCATTAAATTTTCTCATGAAGGATTACATGGGCCGAGCAAGATAAGCAAGGAGAAGAGTTTCTTGGACCTTGTGGTTGAGTTGGAGAACTAAATCTGGTTGCCCCAGA 440  
 Ser Leu Ile Phe Leu Met Lys Asp Tyr Met Gly Arg Gly Lys Ile Ser Lys Glu Lys Ser Phe Leu Asp Leu Val Val Glu Leu Glu Lys Leu Asn Leu Val Ala Pro Asp  
  
 TCAACTGGATTTATTAGAAAAAATGCCTTAAAGAACATCCACAGAAATAGACCTGAAGACAAAAATCCAGAAGTACAAGCAGTCTGTTCAAGGAGCAGGACAAAGTTACAGGA 550  
 Gln Leu Asp Leu Leu Glu Lys Cys Leu Lys Asn Ile His Arg Ile Asp Leu Lys Thr Lys Ile Gln Lys Tyr Lys Gln Ser Val Gln Gly Ala Gly Thr Ser Tyr Arg  
  
 ATGTTCTCCAAGCAGCAATCCAAAAGAGTCTCAAGGATCCTTCAAAATAACTTCAGGCTCCATAATGGGAGAAAGTAAAGAACAAAGACCTTAAGGAACACAGCTTGGCGCTCAA 660  
 Asn Val Leu Gln Ala Ile Gln Lys Ser Leu Lys Asp Pro Ser Asn Asn Phe Arg Leu His Asn Gly Arg Ser Lys Glu Gln Arg Leu Lys Glu Leu Gly Ala Gln  
  
 CAAGAACCCAGTGAAGAAATCCATTACAGGAATCAGAAAGCTTTTTCCTCAGAGCATACCTGAAAGAGAGATACAAGATGAAGAGCAAGCCCTAGGAATCTGCTGATAAT 770  
 Gln Glu Pro Val Lys Lys Ser Ile Gln Glu Ser Glu Ala Phe Leu Pro Gln Ser Ile Pro Glu Glu Arg Tyr Lys Met Lys Ser Lys Pro Leu Gly Ile Cys Leu Ile Ile  
  
 CGATTGCAATTGGCAATGAGACAGAGCTTCTTCGAGACACCTTCACCTCCCTGGGCTATGAAGTCCAGAAATCTTTCGATCTCAGTATGTCATGCTATATCCAGATTCTTG 880  
 Asp Cys Ile Gly Asn Glu Thr Glu Leu Leu Arg Asp Thr Phe Thr Ser Leu Gly Tyr Glu Val Gln Lys Phe Leu His Leu Ser Met His Gly Ile Ser Gln Ile Leu  
  
 GCCAATTTGCCTGTATGCCCGAGCACCGAGACTACGACAGCTTTGTGTGCTCCTGGTGAGCCGAGGAGCTCCACAGAGTGTGTATGGTGTGGATCAGACTCAGG 990  
 Gly Gln Phe Ala Cys Met Pro Glu His Arg Asp Tyr Asp Ser Phe Val Cys Val Leu Val Ser Arg Gly Ser Gln Ser Val Tyr Gly Val Asp Gln Thr His Ser Gly  
  
 CTCCCCCTGCATCACATCAGGAGGATGTTTCATGGGAGATTTCATGCCCTTATCTAGCAGGGAGCCAAAGATGTTTTTTTATTCAGAACTATGTGTGTCAGAGGGCCAGCT 1100  
 Leu Pro Leu His His Ile Arg Arg Met Phe Met Gly Asp Ser Cys Pro Tyr Leu Ala Gly Lys Pro Lys Met Phe Phe Ile Gln Asn Tyr Val Val Ser Glu Gly Gln Leu  
  
 GGAGGACAGCAGCCCTCTTGGAGGTGGATGGGCCAGCGATGAAGAAATGTGGAATTCAGGGCTCAGAAGCGAGGGCTGTGCACAGTTCACCGAGAAGCTGACTTCTTCTGGA 1210  
 Glu Asp Ser Ser Leu Leu Glu Val Asp Gly Pro Ala Met Lys Asn Val Glu Phe Lys Ala Gln Lys Arg Gly Leu Cys Thr Val His Arg Glu Ala Asp Phe Phe Trp  
  
 GCCGTGTACTGCGGACATGTCCCTGCTGGAGCAGTCTCACAGCTCACCATCCCTGTACCTGTCAGTGCCTCTCCAGAAACTGAGACAAGAAAGAAACGCCACCTCC 1320  
 Ser Leu Cys Thr Ala Asp Met Ser Leu Leu Glu Gln Ser His Ser Ser Pro Ser Leu Tyr Leu Gln Cys Leu Ser Gln Lys Leu Arg Gln Glu Arg Lys Arg Pro Leu Leu  
  
 GATCTTCACATTGAACCTCAATGGCTACATGTATGATTGGAACAGCAGAGTTTCTGCCAAGGAGAAAATATTATGTCGTGGCTGCAGCACACTCTGAGAAAAGAACTTATCCT 1430  
 Asp Leu His Ile Glu Leu Asn Gly Tyr Met Tyr Asp Trp Asn Ser Arg Val Ser Ala Lys Glu Lys Tyr Tyr Val Trp Leu Gln His Thr Leu Arg Lys Lys Leu Ile Leu  
  
 CTCCTACACATAA 1443  
 Ser Tyr Thr •

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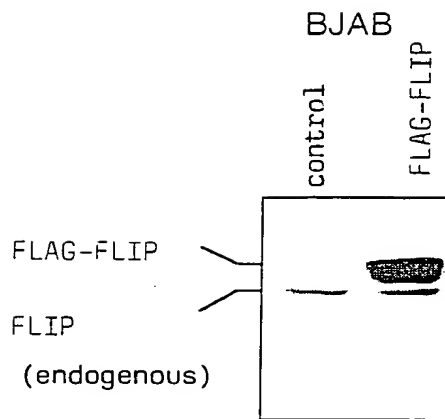
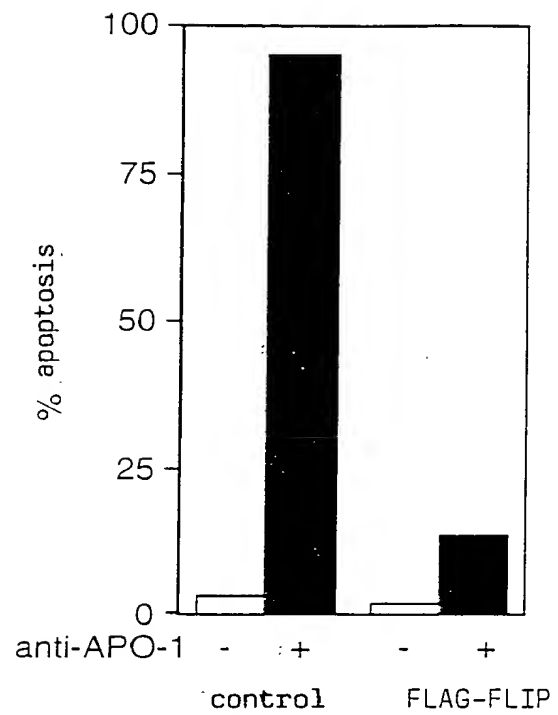
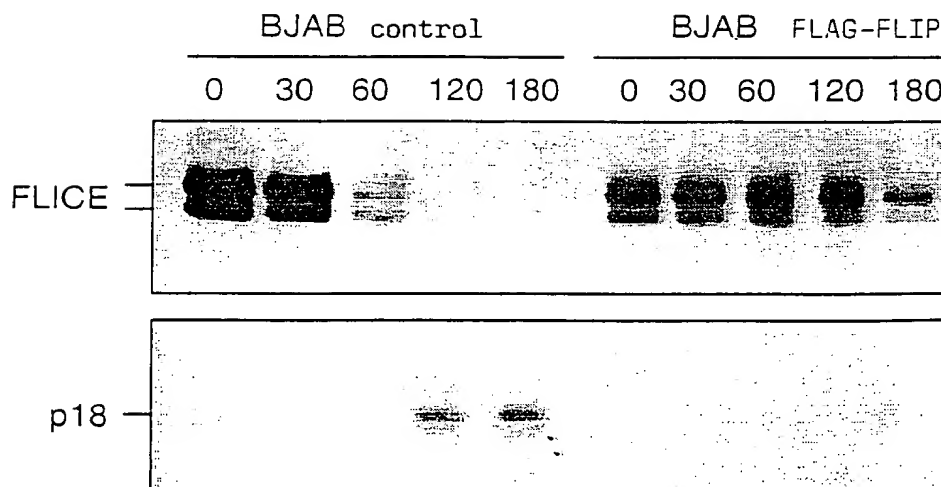
**A****B****C**

Fig. 3